

SEQUENCE LISTING

<110> FUKUCHI, Naoyuki
FUTAKI, Fumie
KITO, Morikazu
SATO, Seiichi
KAJIURA, Takayuki
ONO, Yukitsugu
TANAKA, Akiko
SHINOZAKI, Junko

<120> Substance with Antithrombic Activity and
Method for Detecting Glycocalicin

<130> OP818-PCT

<140> PCT/JP99/00089
<141> 1998-01-13

<150> JP 10-113962
<151> 1998-04-23

<160> 14

<170> PatentIn Ver. 2.0

<210> 1
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 1
atctgtgagg tctccaaagt ggccagccac ctagaa

36

<210> 2
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 2
 atatctagat gtgcccgagg attgtggtt 29

<210> 3
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 3
 ataaagcttc tcgagtcatt taccaggaga gtggga 36

<210> 4
 <211> 684
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(684)

<400> 4
 gtg ccc agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa 48
 Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 1 5 10 15

gta tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc 96
 Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 20 25 30

att act ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag 144
 Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Asp Ile Ser Lys
 35 40 45

gat gat ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg 192
 Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 50 55 60

cac aca gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc 240
 His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 65 70 75 80

cgc tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc 288
 Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 85 90 95

aag gag ttc aaa tgc agg gta aac agt gca gct ttc cct gcc ccc atc 336

Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	
100									105						110	
gag	aaa	acc	atc	tcc	aaa	acc	aaa	ggc	aga	ccg	aag	gct	cca	cag	gtg	384
Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	
115									120					125		
tac	acc	att	cca	cct	ccc	aag	gag	cag	atg	gcc	aag	gat	aaa	gtc	agt	432
Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	
130									135				140			
ctg	acc	tgc	atg	ata	aca	gac	ttc	ttc	cct	gaa	gac	att	act	gtg	gag	480
Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	
145									150			155		160		
tgg	cag	tgg	aat	ggg	cag	cca	gcg	gag	aac	tac	aag	aac	act	cag	ccc	528
Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	
165									170				175			
atc	atg	gac	aca	gat	ggc	tct	tac	ttc	gtc	tac	agc	aag	ctc	aat	gtg	576
Ile	Met	Asp	Thr	Asp	Gly	Ser	Tyr	Phe	Val	Tyr	Ser	Lys	Leu	Asn	Val	
180									185				190			
cag	aag	agc	aac	tgg	gag	gca	gga	aat	act	ttc	acc	tgc	tct	gtg	tta	624
Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	
195									200				205			
cat	gag	ggc	ctg	cac	aac	cac	cat	act	gag	aag	agc	ctc	tcc	cac	tct	672
His	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys	Ser	Leu	Ser	His	Ser	
210									215				220			
cct	ggt	aaa	tga													684
Pro	Gly	Lys														
225																

<210> 5

<211> 227

<212> PRT

<213> Mus musculus

<400> 5

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu

1 5 10 15

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr

20 25 30

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys

35 40 45

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val

50 55 60

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe

65 70 75 80

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 85 90 95
 Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 100 105 110
 Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 115 120 125
 Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 130 135 140
 Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 145 150 155 160
 Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 165 170 175
 Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 180 185 190
 Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 195 200 205
 His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 210 215 220
 Pro Gly Lys
 225

<210> 6

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<220>

<221> CDS

<222> (1)..(1689)

<220>

<221> sig_peptide

<222> (1)..(48)

<220>

<221> mat_peptide

<222> (49)..(1689)

<400> 6

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Met Pro Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro	
-16 -15 -10 -5	
cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac	96
His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn	
1 5 10 15	
tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac	144
Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp	
20 25 30	
aca acc atc ctc cac ctg agt gag aac ctc ctg tac acc ttc tcc ctg	192
Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu	
35 40 45	
gca acc ctg atg cct tac act cgc ctc act cag ctg aac cta gat agg	240
Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg	
50 55 60	
tgc gag ctc acc aag ctc cag gtc gat ggg acg ctg cca gtg ctg ggg	288
Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly	
65 70 75 80	
acc ctg gat cta tcc cac aat cag ctg caa agc ctg ccc ttg cta ggg	336
Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly	
85 90 95	
cag aca ctg cct gct ctc acc gtc ctg gac gtc tcc ttc aac cgg ctg	384
Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu	
100 105 110	
acc tcg ctg cct ctt ggt gcc ctg cgt ggt ctt ggc gaa ctc caa gag	432
Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu	
115 120 125	
ctc tac ctg aaa ggc aat gag ctg aag acc ctg ccc cca ggg ctc ctg	480
Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu	
130 135 140	
acg ccc aca ccc aag ctg gag aag ctc agt ctg gct aac aac aac ttg	528
Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu	
145 150 155 160	
act gag ctc ccc gct ggg ctc ctg aat ggg ctg gag aat ctc gac acc	576
Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr	
165 170 175	
ctt ctc ctc caa gag aac tcg ctg tat aca ata cca aag ggc ttt ttt	624
Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe	
180 185 190	
ggg tcc cac ctc ctg cct ttt gct ttt ctc cac ggg aac ccc tgg tta	672
Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu	
195 200 205	
tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct	720

Cys	Asn	Cys	Glu	Ile	Leu	Tyr	Phe	Arg	Arg	Trp	Leu	Gln	Asp	Asn	Ala	
210				215						220						
gaa	aat	gtc	tac	gta	tgg	aag	caa	ggt	gtg	gac	gtc	aag	gcc	atg	acc	768
Glu	Asn	Val	Tyr	Val	Trp	Lys	Gln	Gly	Val	Asp	Val	Lys	Ala	Met	Thr	
225				230					235			240				
tct	aac	gtg	gcc	agt	gtg	cag	tgt	gac	aat	tca	gac	aag	ttt	ccc	gtc	816
Ser	Asn	Val	Ala	Ser	Val	Gln	Cys	Asp	Asn	Ser	Asp	Lys	Phe	Pro	Val	
				245					250			255				
tac	aaa	aac	cca	gga	aag	ggg	tgc	ccc	acc	ctt	ggt	gat	gaa	ggt	gac	864
Tyr	Lys	Tyr	Pro	Gly	Lys	Gly	Cys	Pro	Thr	Leu	Gly	Asp	Glu	Gly	Asp	
				260					265			270				
aca	gac	cta	tat	gat	tac	tac	cca	gaa	gag	gac	act	gag	ggc	gat	aag	912
Thr	Asp	Leu	Tyr	Asp	Tyr	Tyr	Pro	Glu	Glu	Asp	Thr	Glu	Gly	Asp	Lys	
				275					280			285				
gtg	cgt	gcc	aca	agg	act	gtg	gtc	aag	ttc	ccc	acc	aaa	gcc	cat	aca	960
Val	Arg	Ala	Thr	Arg	Thr	Val	Val	Lys	Phe	Pro	Thr	Lys	Ala	His	Thr	
				290					295			300				
acc	ccc	tgg	ggt	cta	ttc	tac	tca	tgg	tcc	act	gct	tct	cta	gac	gtg	1008
Thr	Pro	Trp	Gly	Leu	Phe	Tyr	Ser	Trp	Ser	Thr	Ala	Ser	Leu	Asp	Val	
				305					310			315			320	
ccc	agg	gat	tgt	ggt	tgt	aag	cct	tgc	ata	tgt	aca	gtc	cca	gaa	gta	1056
Pro	Arg	Asp	Cys	Gly	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	
				325					330			335				
tca	tct	gtc	ttc	atc	ttc	ccc	cca	aag	ccc	aag	gat	gtg	ctc	acc	att	1104
Ser	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	
				340					345			350				
act	ctg	act	cct	aag	gtc	acg	tgt	gtt	gtg	gta	gac	atc	agc	aag	gat	1152
Thr	Leu	Thr	Pro	Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	
				355					360			365				
gat	ccc	gag	gtc	cag	ttc	agc	tgg	ttt	gta	gat	gat	gtg	gag	gtg	cac	1200
Asp	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	
				370					375			380				
aca	gct	cag	acg	caa	ccc	cgg	gag	gag	cag	ttc	aac	agc	act	ttc	cgc	1248
Thr	Ala	Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	
				385					390			395			400	
tca	gtc	agt	gaa	ctt	ccc	atc	atg	cac	cag	gac	tgg	ctc	aat	ggc	aag	1296
Ser	Val	Ser	Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
				405					410			415				
gag	ttc	aaa	tgc	agg	gta	aac	agt	gca	gct	ttc	cct	gcc	ccc	atc	gag	1344
Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	
				420					425			430				
aaa	acc	atc	tcc	aaa	acc	aaa	ggc	aga	ccg	aag	gct	cca	cag	gtg	tac	1392
Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	

435	440	445	
acc att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg			1440
Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu			
450	455	460	
acc tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag tgg			1488
Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp			
465	470	475	480
cag tgg aat ggg cag cca gcg gag aac tac aag aac act cag ccc atc			1536
Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile			
485	490	495	
atg gac aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag			1584
Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln			
500	505	510	
aag agc aac tgg gag gca gga aat act ttc acc tgc tct gtg tta cat			1632
Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His			
515	520	525	
gag ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct			1680
Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro			
530	535	540	
ggt aaa tga			1689
Gly Lys			
545			

<210> 7

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<400> 7

Met Pro Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro			
-16 -15	-10	-5	
His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn			
1	5	10	15
Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp			
20	25	30	
Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu			
35	40	45	
Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg			
50	55	60	

Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly
 65 70 75 80
 Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly
 85 90 95
 Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu
 100 105 110
 Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu
 115 120 125
 Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu
 130 135 140
 Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu
 145 150 155 160
 Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr
 165 170 175
 Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe
 180 185 190
 Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu
 195 200 205
 Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala
 210 215 220
 Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr
 225 230 235 240
 Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val
 245 250 255
 Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp
 260 265 270
 Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys
 275 280 285
 Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr
 290 295 300
 Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Val
 305 310 315 320
 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
 325 330 335
 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
 340 345 350
 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 355 360 365
 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 370 375 380
 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 385 390 395 400
 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys

405	410	415
Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu		
420	425	430
Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr		
435	440	445
Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu		
450	455	460
Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp		
465	470	475
Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile		
485	490	495
Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln		
500	505	510
Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His		
515	520	525
Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro		
530	535	540
Gly Lys		
545		

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 8

agcttaggatc cgagccccaga gggcccacaa

30

<210> 9

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 9

cccaagcttc tcgagacata cctttcattt acccggagtc cggga

44

<210> 10

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of genes of *Mus musculus* and *Homo sapiens*

<220>

<221> CDS

<222> (7)..(708)

<400> 10

ggatcc	gag	ccc	aga	ggg	ccc	aca	atc	aag	ccc	tgt	cct	cca	tgc	aaa	48	
Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys																
1	5									10						
tgc	cca	gca	cct	aac	ctc	ttg	ggt	gga	cca	tcc	gtc	ttc	atc	ttc	cct	96
Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro																
15	20									25					30	
cca	aag	atc	aag	gat	gta	ctc	atg	atc	tcc	ctg	agc	ccc	ata	gtc	aca	144
Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr																
35									40					45		
tgt	gtg	gtg	gtg	gat	gtg	agc	gag	gat	gac	cca	gat	gtc	cag	atc	agc	192
Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser																
50									55					60		
tgg	ttt	gtg	aac	aac	gtg	gaa	gta	cac	aca	gct	cag	aca	caa	acc	cat	240
Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His																
65									70					75		
aga	gag	gat	tac	aac	agt	act	ctc	cgg	gtg	gtc	agt	gcc	ctc	ccc	atc	288
Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile																
80								85					90			
cag	cac	cag	gac	tgg	atg	agt	ggc	aag	gag	ttc	aaa	tgc	aag	gtc	aac	336
Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn																
95								100					105		110	
aac	aaa	gac	ctg	cca	gcg	ccc	atc	gag	aga	acc	atc	tca	aaa	ccc	aaa	384
Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys																
115								120					125			
ggg	tca	gta	aga	gct	cca	cag	gta	tat	gtc	ttg	cct	cca	gaa	gaa	432	
Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu																
130								135					140			
gag	atg	act	aag	aaa	cag	gtc	act	ctg	acc	tgc	atg	gtc	aca	gac	ttc	480
Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe																
145								150					155			
atg	cct	gaa	gac	att	tac	gtg	gag	tgg	acc	aac	aac	ggg	aaa	aca	gag	528

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
 160 165 170 576
 cta aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac
 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
 175 180 185 190 624
 ttc atg tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga
 Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
 195 200 205
 aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac
 Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
 210 215 220
 acg act aag agc ttc tcc cgg act ccg ggt aaa tgaaaggat gtctcgagaa 725
 Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 225 230 729
 gctt

<210> 11

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<400> 11
 Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
 1 5 10 15
 Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
 20 25 30
 Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
 35 40 45
 Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
 50 55 60
 Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
 65 70 75 80
 Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
 85 90 95
 Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
 100 105 110
 Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
 115 120 125
 Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Met

12/17

130	135	140
Thr Lys Lys Gln Val	Thr Leu Thr Cys Met Val	Thr Asp Phe Met Pro
145	150	155
Glu Asp Ile Tyr Val	Glu Trp Thr Asn Asn	Gly Lys Thr Glu Leu Asn
165	170	175
Tyr Lys Asn Thr Glu Pro Val	Leu Asp Ser Asp Gly Ser	Tyr Phe Met
180	185	190
Tyr Ser Lys Leu Arg Val	Glu Lys Lys Asn Trp Val	Glu Arg Asn Ser
195	200	205
Tyr Ser Cys Ser Val Val	His Glu Gly Leu His Asn His	His Thr Thr
210	215	220
Lys Ser Phe Ser Arg Thr Pro	Gly Lys	
225	230	

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

agctatatctag acgagccca agggccca

30

<210> 13

<211> 1707

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<220>

<221> CDS

<222> (1)..(1707)

<220>

<221> sig_peptide

<222> (1)..(48)

<220>

<221> mat_peptide
<222> (49)..(1704)

<400> 13	48
atg cct ctc ctc ctc ttg ctg ctc ctg cca agc ccc tta cac cac ccc Met Pro Leu Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro	
-16 -15 -10 -5	
cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn	96
1 5 10 15	
tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp	144
20 25 30	
aca acc atc ctc cac ctg agt gag aac ctc ctg tac acc ttc tcc ctg Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu	192
35 40 45	
gca acc ctg atg cct tac act cgc ctc act cag ctg aac cta gat agg Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg	240
50 55 60	
tgc gag ctc acc aag ctc cag gtc gat ggg acg ctg cca gtg ctg ggg Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly	288
65 70 75 80	
acc ctg gat cta tcc cac aat cag ctg caa agc ctg ccc ttg cta ggg Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly	336
85 90 95	
cag aca ctg cct gct ctc acc gtc ctg gac gtc tcc ttc aac cgg ctg Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu	384
100 105 110	
acc tcg ctg cct ctt ggt gcc ctg cgt ggt ctt ggc gaa ctc caa gag Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu	432
115 120 125	
ctc tac ctg aaa ggc aat gag ctg aag acc ctg ccc cca ggg ctc ctg Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu	480
130 135 140	
acg ccc aca ccc aag ctg gag aag ctc agt ctg gct aac aac aac ttg Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu	528
145 150 155 160	
act gag ctc ccc gct ggg ctc ctg aat ggg ctg gag aat ctc gac acc Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr	576
165 170 175	
ctt ctc ctc caa gag aac tcg ctg tat aca ata cca aag ggc ttt ttt Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe	624
180 185 190	

ggg tcc cac ctc ctg cct ttt gct ttt ctc cac ggg aac ccc tgg tta	672
Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu	
195 200 205	
tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct	720
Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala	
210 215 220	
gaa aat gtc tac gta tgg aag caa ggt gtg gac gtc aag gcc atg acc	768
Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr	
225 230 235 240	
tct aac gtg gcc agt gtg cag tgt gac aat tca gac aag ttt ccc gtc	816
Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val	
245 250 255	
tac aaa tac cca gga aag ggg tgc ccc acc ctt ggt gat gaa ggt gac	864
Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp	
260 265 270	
aca gac cta tat gat tac tac cca gaa gag gac act gag ggc gat aag	912
Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys	
275 280 285	
gtg cgt gcc aca agg act gtg gtc aag ttc ccc acc aaa gcc cat aca	960
Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr	
290 295 300	
acc ccc tgg ggt cta ttc tac tca tgg tcc act gct tct cta gac gag	1008
Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Glu	
305 310 315 320	
ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa tgc cca gca	1056
Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala	
325 330 335	
cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag atc	1104
Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile	
340 345 350	
aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg	1152
Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val	
355 360 365	
gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt gtg	1200
Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val	
370 375 380	
aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat	1248
Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp	
385 390 395 400	
tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag	1296
Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln	
405 410 415	
gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac	1344

Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp				
420	425	430		
ctg cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta				1392
Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val				
435	440	445		
aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg act				1440
Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Glu Glu Glu Met Thr				
450	455	460		
aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct gaa				1488
Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu				
465	470	475	480	
gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac tac				1536
Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr				
485	490	495		
aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg tac				1584
Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr				
500	505	510		
agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc tac				1632
Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr				
515	520	525		
tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg act aag				1680
Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys				
530	535	540		
agc ttc tcc cgg act ccg ggt aaa tga				1707
Ser Phe Ser Arg Thr Pro Gly Lys				
545	550			

<210> 14

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of
genes of *Mus musculus* and *Homo sapiens*

<400> 14

Met Pro Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro
-16 -15 -10 -5His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn
1 5 10 15Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp
20 25 30

Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu
 35 40 45
 Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg
 50 55 60
 Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly
 65 70 75 80
 Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly
 85 90 95
 Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu
 100 105 110
 Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu
 115 120 125
 Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu
 130 135 140
 Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu
 145 150 155 160
 Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr
 165 170 175
 Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe
 180 185 190
 Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu
 195 200 205
 Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala
 210 215 220
 Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr
 225 230 235 240
 Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val
 245 250 255
 Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp
 260 265 270
 Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys
 275 280 285
 Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr
 290 295 300
 Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Glu
 305 310 315 320
 Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala
 325 330 335
 Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile
 340 345 350
 Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val
 355 360 365
 Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val

370	375	380
Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp		
385	390	395
Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln		
405	410	415
Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp		
420	425	430
Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val		
435	440	445
Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr		
450	455	460
Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu		
465	470	475
Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr		
485	490	495
Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr		
500	505	510
Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr		
515	520	525
Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys		
530	535	540
Ser Phe Ser Arg Thr Pro Gly Lys		
545	550	